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cagaagttca aaggcaaggc cacattgact gcagacaaat cctccagcac agcctacatg
                                                                      300
cagctcagca gcctgacatc tgaggactct gcggtctatt actgtgcaag atcgacttac
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Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
Ala Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
                           4.0
                                                45
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
                                        75
                    70
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
                                                    110
           100
                               105
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
                           120
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala
                       135
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<222> (1)..(29)
<223> r is g or a
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ggstgttgtg ctagctgmrg agacrgtga
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